

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 26.8605 Seconds

(Without alignments)
843.812 Million cell updates/sec

Title: US-09-622-613b-24

Perfect score: 601

Sequence: 1 SMNATFOOKHIIINPTICNT.....ICVKCENQYVHFGIGRCP.110

Scoring table: BLCSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP.TREMBL_21:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.protozoa:*
13: sp.virus:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriophage:*
17: sp.archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586.5	97.6	133	09PWR7	09PWR7 rana catesb
2	555.5	92.4	133	098SM0	098SM0 rana catesb
3	482.5	80.3	132	098SM2	098SM2 rana catesb
4	473.5	78.8	133	098SL9	098SL9 rana catesb
5	466.5	77.6	133	098SL8	098SL8 rana catesb
6	443.5	73.8	132	098SM1	098SM1 rana catesb
7	371	61.7	132	09DF78	09DF78 rana catesb
8	276.5	46.0	127	0918V8	0918V8 rana pipien
9	272.5	45.3	127	08UVX5	08UVX5 rana pipien
10	241	40.1	129	09DFY6	09DFY6 rana catesb
11	224.5	37.4	128	09DFY8	09DFY8 rana catesb
12	221.5	36.9	128	09DFY7	09DFY7 rana catesb
13	212.5	35.4	128	09DFY5	09DFY5 rana catesb
14	158	26.3	169	09W738	09W738 xenopus lae
15	131	21.8	170	09BEC1	09BEC1 tragus ja
16	126	21.0	150	08VD94	08VD94 beryllus bo

17	125.5	20.9	163	6	09BDC2	09BDC2 antilocapra
18	124.5	20.7	116	6	09VCO	09VCO sus scrofa
19	124	20.6	150	11	08VD88	08VD88 ratus norv
20	122.5	20.4	144	6	09BH14	09BH14 antilocapra
21	120	20.0	150	11	08VD92	08VD92 ratus exul
22	116.5	19.4	152	11	08VD89	08VD89 ratus norv
23	115.5	19.2	119	6	09TV33	09TV33 bos taurus
24	114.5	19.1	124	6	095NE6	095NE6 bubalus bub
25	112.5	18.7	149	11	08VD95	08VD95 beryllus bo
26	112	18.6	134	6	09BD89	09BD89 tragus ja
27	111.5	18.6	152	11	08VD84	08VD84 ratus tliom
28	111.5	18.6	156	6	08S005	08S005 lagochrix 1
29	110.5	18.4	119	6	09TV30	09TV30 saginus oe
30	110.5	18.4	119	6	09TV28	09TV28 eulimur ful
31	110.5	18.4	124	6	09TSF2	09TSF2 bos taurus
32	109.5	18.2	142	6	09BEC3	09BEC3 tragus ja
33	109.5	18.2	156	6	08S006	08S006 ateles geot
34	109	18.1	124	6	09BEC2	09BEC2 tragus ja
35	108.5	18.1	156	6	08S008	08S008 salimiri sci
36	108.5	18.1	156	6	08S007	08S007 saginus oe
37	107.5	17.9	152	11	08VD90	08VD90 ratus fusc
38	106.5	17.7	116	6	097933	097933 phocoenide
39	106.5	17.7	149	11	08VD93	08VD93 ratus exul
40	105.5	17.6	116	6	097934	097934 pseudorca c
41	105.5	17.6	119	6	09TS06	09TS06 ceropithec
42	105.5	17.6	157	11	09JKJ4	09JKJ4 meriones un
43	105	17.5	158	6	08SPY2	08SPY2 callithrix
44	104.5	17.4	119	6	09TV32	09TV32 gorilla gor
45	104.5	17.4	124	6	09XS40	09XS40 camelus bac

ALIGNMENTS

RESULT 1
09PWR7 PRELIMINARY; PRT: 133 AA.
AC 09PWR7:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Ribonuclease precursor.
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.,
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
DR EMBL: AF039104; AAD10702.1;
DR HSSP: P11916; 18C4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_PC; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL. 1 22 POTENTIAL.
FT CHAIN 23 133 RIBONUCLEASE.
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16FOC CRC64;
Query Match 97.6%; Score 586.5; DB 13; Length 133;
Best Local Similarity 99.1%; Pred. No. 2.7e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
OY 2 NMATFOOKHIIINPTICNTIMDNIIYVGQCKRVNTEIISATVKAICGVINNVL 60

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Db      24  NMAFFQOKHIINTPIT-CNTIMDNNTIYVGGCKRVNTFISSATTVAICTGVINMVL 83
OY      61  STTRFQOLNCTRTSITPRPCPYSSRTETNYICVGCENQYPVHFAGIGRCP 110
Db      84  STTRFQOLNCTRTSITPRPCPYSSRTETNYICVGCENQYPVHFAGIGRCP 133

RESULT 2
O98SMO  PRELIMINARY: PRT: 133 AA.
ID      098SMO:
AC      01-JUN-2001 (Tremblrel. 17, Created)
DT      01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT      01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE      RNase A-type ribonuclease rc208 precursor.
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
OX      NCBI_TaxID=8400;
RN      11
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21539506; PubMed=11683320;
RT      "Rapid diversification of RNase A superfamily ribonuclease from the
RT      bullfrog, Rana catesbeiana."
RL      J. Mol. Evol. 53:31-38(2001).
DR      HSSP; P11916; 1BC4.
DR      HSSP; AF351209; AAK30255.1; -.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam; PF00074; rnasea; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_PC; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW      Signal.
FT      SIGNAL.
SQ      SEQUENCE 133 AA: 14628 MW: 877CF122C3499E02 CRC64;

Query Match 92.4%; Score 555.5; DB 13; Length 133;
Best Local Similarity 94.5%; Pred. No. 1.1e-56;
Matches 104; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY      2  NMAFFQOKHIINTPIT-CNTIMDNNTIYVGGCKRVNTFISSATTVAICTGVINMVL 60
Db      24  NMAFFQOKHIINTPIT-CNTIMDNNTIYVGGCKRVNTFISSATTVAICTGVINMVL 83
OY      61  STTRFQOLNCTRTSITPRPCPYSSRTETNYICVGCENQYPVHFAGIGRCP 110
Db      84  STTRFQOLNCTRTSITPRPCPYSSRTETNYICVGCENQYPVHFAGIGRCP 133

RESULT 3
O98SMO  PRELIMINARY: PRT: 132 AA.
ID      098SMO:
AC      01-JUN-2001 (Tremblrel. 17, Created)
DT      01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT      01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE      RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
OX      NCBI_TaxID=8400;
RN      11
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21539506; PubMed=11683320;
RT      "Rapid diversification of RNase A superfamily ribonuclease from the
RT      bullfrog, Rana catesbeiana."
RL      J. Mol. Evol. 53:31-38(2001).
DR      HSSP; P11916; 1BC4.
DR      HSSP; AF351209; AAK30255.1; -.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam; PF00074; rnasea; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_PC; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW      Signal.
FT      SIGNAL.
SQ      SEQUENCE 133 AA: 14615 MW: C8785B236B2654E CRC64;

Query Match 78.8%; Score 473.5; DB 13; Length 133;
Best Local Similarity 78.2%; Pred. No. 3.4e-47;
Matches 86; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

OY      2  NMAFFQOKHIINTPIT-CNTIMDNNTIYVGGCKRVNTFISSATTVAICTGVINMVL 60
Db      24  NMAFFQOKHIINTPIT-CNTIMDNNTIYVGGCKRVNTFISSATTVAICTGVINMVL 83
OY      61  STTRFQOLNCTRTSITPRPCPYSSRTETNYICVGCENQYPVHFAGIGRCP 110
Db      84  STTRFQOLNCTRTSITPRPCPYSSRTETNYICVGCENQYPVHFAGIGRCP 133

RESULT 4
O98SL9  PRELIMINARY: PRT: 133 AA.
ID      098SL9:
AC      01-JUN-2001 (Tremblrel. 17, Created)
DT      01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT      01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE      RNase A-type ribonuclease rc212 precursor.
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
OX      NCBI_TaxID=8400;
RN      11
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21539506; PubMed=11683320;
RT      "Rapid diversification of RNase A superfamily ribonuclease from the
RT      bullfrog, Rana catesbeiana."
RL      J. Mol. Evol. 53:31-38(2001).
DR      HSSP; P11916; 1BC4.
DR      HSSP; AF351210; AAK30256.1; -.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam; PF00074; rnasea; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_PC; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW      Signal.
FT      SIGNAL.
SQ      SEQUENCE 133 AA: 14615 MW: C8785B236B2654E CRC64;

Query Match 80.3%; Score 482.5; DB 13; Length 132;
Best Local Similarity 84.3%; Pred. No. 3e-48;
Matches 91; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

OY      3  WATFQOKHIINTPIT-CNTIMDNNTIYVGGCKRVNTFISSATTVAICTGVINMVL 61
Db      25  WATFQOKHIINTPIT-CNTIMDNNTIYVGGCKRVNTFISSATTVAICTGVINMVL 84
OY      62  TTRFQOLNCTRTSITPRPCPYSSRTETNYICVGCENQYPVHFAGIGRCP 109
Db      85  PTRFQOLNCTRTSITPRPCPYSSRTETNYICVGCENQYPVHFAGIGRCP 132

RESULT 5
O98SL8  PRELIMINARY: PRT: 133 AA.
ID      098SL8:
AC      01-JUN-2001 (Tremblrel. 17, Created)
DT      01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT      01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE      RNase A-type ribonuclease rc212 precursor.
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
OX      NCBI_TaxID=8400;
RN      11
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21539506; PubMed=11683320;
RT      "Rapid diversification of RNase A superfamily ribonuclease from the
RT      bullfrog, Rana catesbeiana."
RL      J. Mol. Evol. 53:31-38(2001).
DR      HSSP; P11916; 1BC4.
DR      HSSP; AF351210; AAK30256.1; -.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam; PF00074; rnasea; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_PC; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW      Signal.
FT      SIGNAL.
SQ      SEQUENCE 133 AA: 14615 MW: C8785B236B2654E CRC64;

Query Match 78.8%; Score 473.5; DB 13; Length 133;
Best Local Similarity 78.2%; Pred. No. 3.4e-47;
Matches 86; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

OY      2  NMAFFQOKHIINTPIT-CNTIMDNNTIYVGGCKRVNTFISSATTVAICTGVINMVL 60
Db      24  NMAFFQOKHIINTPIT-CNTIMDNNTIYVGGCKRVNTFISSATTVAICTGVINMVL 83
OY      61  STTRFQOLNCTRTSITPRPCPYSSRTETNYICVGCENQYPVHFAGIGRCP 110
Db      84  STTRFQOLNCTRTSITPRPCPYSSRTETNYICVGCENQYPVHFAGIGRCP 133

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ID 098SL8 PRELIMINARY; PRT; 133 AA.

AC 098SL8; 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE RNase A-type ribonuclease rc213 precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

NCBI_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

RL bullfrog, *Rana catesbeiana*."

EMBL: AF351211; AAF30257.1; -

DR HSSP; P11916; IBC4.

DR InterPro: IPR01427; RNaseA.

DR Pfam: PF00074; rnaasea; 1.

DR Prodom: PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_PC; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.

KW SIGNAL.

FT SIGNAL.

SO SEQUENCE 133 AA; 14590 MW; 8B40B9A4FA5B943 CRC64;

Query Match 77.68; Score 466.5; DB 13; Length 133;

Best Local Similarity 76.48; Pred. No. 2.2e-46;

Matches 84; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

QY 2 NMATPOOKHIIINPIT-CNTIMDNNTIYVGCKRVNFTFISSATYKATCTGVINNVL 60

Db 24 NMATPOKHITNTSSINCIMNLSIYVGCKKVTFTFIASSATYKATCTGVINNVL 83

QY 61 STTRPOLNCTRTSTPRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 110

Db 84 STTRPOLDICTRTIFITPRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 133

RESULT 6

Q98SM1 PRELIMINARY; PRT; 132 AA.

AC 098SM1; 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE RNase A-type ribonuclease rc204 precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

NCBI_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

RL bullfrog, *Rana catesbeiana*."

EMBL: AF351208; AAF30254.1; -

DR HSSP; P11916; IBC4.

DR InterPro: IPR01427; RNaseA.

DR Pfam: PF00074; rnaasea; 1.

DR Prodom: PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_PC; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.

KW SIGNAL.

FT SIGNAL.

SO SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 73.88; Score 443.5; DB 13; Length 132;

Best Local Similarity 78.08; Pred. No. 1e-43;

Matches 85; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 2 NMATPOOKHIIINPIT-CNTIMDNNTIYVGCKRVNFTFISSATYKATCTGVINNVL 60

Db 24 DWTFPOOKHLPSTSSIDCNTIMDKDIYVGCKKVTFTFISSATYKATCTGVINNVL 83

QY 61 STTRPOLNCTRTSTPRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 109

Db 84 STTRPOLXNTRFTITRPRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 132

RESULT 7

Q9DF78 PRELIMINARY; PRT; 132 AA.

AC 09DF78; 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE RC-Nase1 ribonuclease precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

NCBI_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20512555; PubMed=11058105;

RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;

RT "Purification and cloning of cytoxic ribonucleases from *Rana*

RL catesbeiana (bullfrog)."

EMBL: AF288642; AAG30414.2; -

DR HSSP; P11916; IBC4.

DR InterPro: IPR01427; RNaseA.

DR Pfam: PF00074; rnaasea; 1.

DR Prodom: PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_PC; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.

KW SIGNAL.

FT SIGNAL.

SO SEQUENCE 132 AA; 14625 MW; D8D9A517452FB53 CRC64;

Query Match 61.78; Score 371; DB 13; Length 132;

Best Local Similarity 65.58; Pred. No. 2.6e-35;

Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 NMATPOOKHIIINPIT-CNTIMDNNTIYVGCKRVNFTFISSATYKATCTGVINNVL 59

Db 23 NMAKFEKHITSTSSIDCNTIMDKAIYVGCKKERTFTFISSBDNKAICSGVSPRKE 82

QY 60 LSTRPOLNCTRTSTPRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 109

Db 83 LSTRPOLNCTIRDSITPRPCPYSSRPTETNYICVCKENQYVHFAGIGRC 132

RESULT 8

Q918V8 PRELIMINARY; PRT; 127 AA.

AC 0918V8; 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE Onconase variant rapiri precursor.

OS Rana pipiens (Northern Leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

NCBI_TaxID=8404;

RESULT 13

RA Kinoshita N., Kirschner M.W.;

